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Application Number	09/903,378
Filing Date	July 10, 2001
First Named Inventor	CHIRINO, Arthur J.
Group Art Unit	1645
Examiner Name	
Attorney Docket Number	A-69566-1/RFT/RMS/RMK

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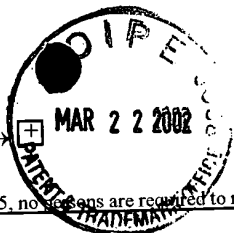
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OTHER PRIOR ART - NON PATENT LITERATURE DOCUMENTS

Examiner Initials*	Cite No. ¹	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T ²
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	C4	BOESTEANU, A. et al., "A molecular basis for how a single TCR interfaces multiple ligands," <i>J Immunol.</i> 1998 Nov 1;161(9):4719-27	
	C5	BOWIE, J.U. et al., "A method to identify protein sequences that fold into a known three-dimensional structure," <i>Science.</i> 1991 Jul 12;253(5016):164-70	
	C6	BRUSIC, V., et al., "MHCPEP, a database of MHC-binding peptides: update 1997," <i>Nucleic Acids Res.</i> 1998 Jan 1;26(1):368-71	
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	C9	BUUS, S., "Description and prediction of peptide-MHC binding: the 'human MHC project'," <i>Curr Opin Immunol.</i> 1999 Apr;11(2):209-13	
	C10	CHICZ, R.M. et al., "Predominant naturally processed peptides bound to HLA-DR1 are derived from MHC-related molecules and are heterogeneous in size," <i>Nature.</i> 1992 Aug 27;358(6389):764-8	
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	C13	de LALLA, C. et al., "Cutting edge: identification of novel T cell epitopes in Lol p5a by computational prediction," <i>J Immunol.</i> 1999 Aug 15;163(4):1725-9	
	C14	DESJARLAIS, J.R. and HANDEL, T.M., "De novo design of the hydrophobic cores of proteins," <i>Protein Sci.</i> 1995 Oct;4(10):2006-18	
	C15	FLECKENSTEIN, B. et al., "New ligands binding to the human leukocyte antigen class II molecule DRB1*0101 based on the activity pattern of an undecapeptide library," <i>Eur J Biochem.</i> 1996 Aug 15;240(1):71-7	
	C16	FREMONT, D.H., et al., "Crystal structures of two viral peptides in complex with murine MHC class I H-2Kb," <i>Science.</i> 1992 Aug 14;257(5072):919-27	
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MM	C18	HAMMER, J. et al., "Precise prediction of major histocompatibility complex class II-peptide interaction based on peptide side chain scanning," <i>J Exp Med.</i> 1994 Dec 1;180(6):2353-8	

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mm	C19	HAMMER, J. et al., "High-affinity binding of short peptides to major histocompatibility complex class II molecules by anchor combinations." <i>Proc Natl Acad Sci U S A</i> . 1994 May 10;91(10):4456-60	
	C20	HAMMER, J. "New methods to predict MHC-binding sequences within protein antigens." <i>Curr Opin Immunol</i> . 1995 Apr;7(2):263-9	
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	C25	HIEMSTRA, H.S. et al., "Antigen arrays in T cell immunology." <i>Curr Opin Immunol</i> . 2000 Feb;12(1):80-4	
	C26	HOLLON, T., "Exposing Epitopes Without Exposing People," <i>The Scientist</i> 15(11):14, May 28, 2001	
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	C32	MADDEN, DR., "The three-dimensional structure of peptide-MHC complexes," <i>Annu Rev Immunol</i> . 1995;13:587-622	
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	C34	MALLIOS, RR. "Iterative stepwise discriminant analysis: a meta-algorithm for detecting quantitative sequence motifs." <i>J Comput Biol</i> . 1998 Winter;5(4):703-11	
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mtg	C37	MEISTER, G.E., et al., "Two novel T cell epitope prediction algorithms based on MHC-binding motifs; comparison of predicted and published epitopes from Mycobacterium tuberculosis and HIV protein sequences," <i>Vaccine</i> . 1995 Apr;13(6):581-91	
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mtg	C53	SIDNEY, J. et al., "Definition of a DQ3.1-specific binding motif." <i>J Immunol</i> . 1994 May 1;152(9):4516-25	

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